

SEQUENCE LISTING

<110> YAMAMOTO, Kazuo
Sumitomo Corporation

<120> Carbohydrate library constructed by Gene Alteration of Cargo
Receptors

<130> PH-1716PCT

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<150> JP 2002-238559

<151> 2002-08-19

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<170> PatentIn Ver. 2.0

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<212> DNA

<213> Homo sapiens

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<222> (22)..(1554)

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<221> sig_peptide

<222> (22)..(112)

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gcc	aga	gtt	cgg	ccg	ctg	ttc	tgc	gcc	ttg	ctg	ctg	tca	ctc	ggt	cgc	99
Ala	Arg	Val	Arg	Pro	Leu	Phe	Cys	Ala	Leu	Leu	Leu	Ser	Leu	Gly	Arg	
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ttc	gtc	cgg	ggc	gac	ggc	gtg	gga	gga	gac	ccc	gcg	gtc	gcg	ttg	cca	147
Phe	Val	Arg	Gly	Asp	Gly	Val	Gly	Gly	Asp	Pro	Ala	Val	Ala	Leu	Pro	

30	35	40	
cat cgc cgt ttc gag tac aaa tac agc ttc aag ggg ccg cac ctg gtg			195
His Arg Arg Phe Glu Tyr Lys Tyr Ser Phe Lys Gly Pro His Leu Val			
45	50	55	
cag agc gac ggg acc gtg ccc ttc tgg gcc cac gcg ggg aat gct att			243
Gln Ser Asp Gly Thr Val Pro Phe Trp Ala His Ala Gly Asn Ala Ile			
60	65	70	
cca agt tca gat caa att cga gta gca cca tct tta aaa agc caa aga			291
Pro Ser Ser Asp Gln Ile Arg Val Ala Pro Ser Leu Lys Ser Gln Arg			
75	80	85	90
ggc tca gtg tgg aca aag aca aaa gcg gcc ttt gag aac tgg gaa gtt			339
Gly Ser Val Trp Thr Lys Thr Lys Ala Ala Phe Glu Asn Trp Glu Val			
95	100	105	
gag gtg aca ttt cga gtg act gga aga ggt cga att gga gct gat ggc			387
Glu Val Thr Phe Arg Val Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly			
110	115	120	
cta gca att tgg tat gca gaa aat caa ggc ttg gag ggc cct gtg ttt			435
Leu Ala Ile Trp Tyr Ala Glu Asn Gln Gly Leu Glu Gly Pro Val Phe			
125	130	135	
gga tca gct gat ctg tgg aat ggt gtt gga ata ttt ttt gat act ttt			483
Gly Ser Ala Asp Leu Trp Asn Gly Val Gly Ile Phe Phe Asp Thr Phe			
140	145	150	
gac aat gat gga aag aaa aat aat cct gct ata gta att ata ggc aac			531
Asp Asn Asp Gly Lys Lys Asn Asn Pro Ala Ile Val Ile Ile Gly Asn			
155	160	165	170
aat gga caa atc cat tat gac cat caa aat gac ggg gct agt caa gct			579
Asn Gly Gln Ile His Tyr Asp His Gln Asn Asp Gly Ala Ser Gln Ala			
175	180	185	
ttg gca agt tgc cag agg gac ttc cgc aac aaa ccc tat cct gtc cga			627
Leu Ala Ser Cys Gln Arg Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg			
190	195	200	
gca aag att acc tat tac cag aac aca ctg aca gta atg atc aat aat			675
Ala Lys Ile Thr Tyr Tyr Gln Asn Thr Leu Thr Val Met Ile Asn Asn			
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ggc ttt aca cca gat aaa aat gat tat gaa ttt tgt gcc aaa gtg gaa	723
Gly Phe Thr Pro Asp Lys Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu	
220 225 230	
aat atg att atc cct gca caa ggg cat ttt gga ata tct gct gca act	771
Asn Met Ile Ile Pro Ala Gln Gly His Phe Gly Ile Ser Ala Ala Thr	
235 240 245 250	
gga ggt ctt gca gat gac cat gat gtc ctt tct ttt ctg act ttc cag	819
Gly Gly Leu Ala Asp Asp His Asp Val Leu Ser Phe Leu Thr Phe Gln	
255 260 265	
ttg act gaa cct gga aaa gag ccg ccc aca cca gat aaa gaa att tcg	867
Leu Thr Glu Pro Gly Lys Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser	
270 275 280	
gaa aag gaa aaa gaa aag tat cag gag gaa ttt gag cac ttt caa caa	915
Glu Lys Glu Lys Glu Lys Tyr Gln Glu Glu Phe Glu His Phe Gln Gln	
285 290 295	
gaa ttg gat aaa aaa aaa gag gaa ttc cag aag ggc cac ccc gac ctc	963
Glu Leu Asp Lys Lys Lys Glu Glu Phe Gln Lys Gly His Pro Asp Leu	
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Gln Gly Gln Pro Ala Glu Glu Ile Phe Glu Ser Val Gly Asp Arg Glu	
315 320 325 330	
cta aga caa gtc ttt gaa gga cag aat cgt att cat ctt gaa atc aag	1059
Leu Arg Gln Val Phe Glu Gly Gln Asn Arg Ile His Leu Glu Ile Lys	
335 340 345	
cag ctg aac cgg cag tta gat atg att ctt gat gaa cag aga aga tat	1107
Gln Leu Asn Arg Gln Leu Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr	
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gtc tct tcc tta aca gag gaa atc tct aaa aga gga gca gga atg cct	1155
Val Ser Ser Leu Thr Glu Glu Ile Ser Lys Arg Gly Ala Gly Met Pro	
365 370 375	
ggg cag cat ggg cag att act caa caa gaa ctg gat act gtt gtg aaa	1203
Gly Gln His Gly Gln Ile Thr Gln Gln Glu Leu Asp Thr Val Val Lys	
380 385 390	

act cag cat gag att ctg aga caa gta aat gaa atg aaa aat tcc atg 1251
 Thr Gln His Glu Ile Leu Arg Gln Val Asn Glu Met Lys Asn Ser Met
 395 400 405 410

agt gaa acc gtc aga ctg gtc agt gga atg cag cac cct ggc tct gct 1299
 Ser Glu Thr Val Arg Leu Val Ser Gly Met Gln His Pro Gly Ser Ala
 415 420 425

gga ggc gtc tat gag aca aca cag cac ttc att gac atc aaa gag cac 1347
 Gly Gly Val Tyr Glu Thr Thr Gln His Phe Ile Asp Ile Lys Glu His
 430 435 440

ctg cac ata gta aag agg gac ata gat aac tta gtg cag cga aat atg 1395
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cca tca aat gaa aag ccg aaa tgc cca gaa cta cca cca ttt cca tca 1443
 Pro Ser Asn Glu Lys Pro Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser
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tgt ttg tct acg gtc cac ttc att ata ttt gtt gtg gtg caa act gta 1491
 Cys Leu Ser Thr Val His Phe Ile Ile Phe Val Val Val Gln Thr Val
 475 480 485 490

tta ttc att ggt tat atc atg tat agg tct cag caa gaa gca gct gcc 1539
 Leu Phe Ile Gly Tyr Ile Met Tyr Arg Ser Gln Gln Glu Ala Ala Ala
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aaa aaa ttc ttt tga ctaccatttt cctgtgtact tcatctatatt gtgtacaaaa 1594
 Lys Lys Phe Phe
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tgagtcgttt tgagggaatt taagtattta aattgcttca tagtctaaat tattaatttt 1654

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tcagtatgat gcagcctctg agcagaatat tgaccagtaa gagggtaaataa aaagtggggg 1834

caaccctgga tatgaatggt accccctaag tctccaatat tgcaggtttc cctgtataac 1894

gtaaacacac ttgccctcat gcctcccaga atatgaggtc taattaagaa gtccatcagg 1954

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 35 40 45
 Lys Tyr Ser Phe Lys Gly Pro His Leu Val Gln Ser Asp Gly Thr Val
 50 55 60

Pro Phe Trp Ala His Ala Gly Asn Ala Ile Pro Ser Ser Asp Gln Ile
 65 70 75 80

Arg Val Ala Pro Ser Leu Lys Ser Gln Arg Gly Ser Val Trp Thr Lys
 85 90 95

Thr Lys Ala Ala Phe Glu Asn Trp Glu Val Glu Val Thr Phe Arg Val
 100 105 110

Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly Leu Ala Ile Trp Tyr Ala
 115 120 125

Glu Asn Gln Gly Leu Glu Gly Pro Val Phe Gly Ser Ala Asp Leu Trp
 130 135 140

Asn Gly Val Gly Ile Phe Phe Asp Thr Phe Asp Asn Asp Gly Lys Lys
 145 150 155 160

Asn Asn Pro Ala Ile Val Ile Ile Gly Asn Asn Gly Gln Ile His Tyr
 165 170 175

Asp His Gln Asn Asp Gly Ala Ser Gln Ala Leu Ala Ser Cys Gln Arg
 180 185 190

Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg Ala Lys Ile Thr Tyr Tyr
 195 200 205

Gln Asn Thr Leu Thr Val Met Ile Asn Asn Gly Phe Thr Pro Asp Lys
 210 215 220

Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu Asn Met Ile Ile Pro Ala
 225 230 235 240

Gln Gly His Phe Gly Ile Ser Ala Ala Thr Gly Gly Leu Ala Asp Asp
 245 250 255

His Asp Val Leu Ser Phe Leu Thr Phe Gln Leu Thr Glu Pro Gly Lys
 260 265 270

Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser Glu Lys Glu Lys Glu Lys
 275 280 285

Tyr Gln Glu Glu Phe Glu His Phe Gln Gln Glu Leu Asp Lys Lys Lys
 290 295 300

Glu Glu Phe Gln Lys Gly His Pro Asp Leu Gln Gly Gln Pro Ala Glu
305 310 315 320

Glu Ile Phe Glu Ser Val Gly Asp Arg Glu Leu Arg Gln Val Phe Glu
325 330 335

Gly Gln Asn Arg Ile His Leu Glu Ile Lys Gln Leu Asn Arg Gln Leu
340 345 350

Asp Met Ile Leu Asp Glu Gln Arg Arg Tyr Val Ser Ser Leu Thr Glu
355 360 365

Glu Ile Ser Lys Arg Gly Ala Gly Met Pro Gly Gln His Gly Gln Ile
370 375 380

Thr Gln Gln Glu Leu Asp Thr Val Val Lys Thr Gln His Glu Ile Leu
385 390 395 400

Arg Gln Val Asn Glu Met Lys Asn Ser Met Ser Glu Thr Val Arg Leu
405 410 415

Val Ser Gly Met Gln His Pro Gly Ser Ala Gly Gly Val Tyr Glu Thr
420 425 430

Thr Gln His Phe Ile Asp Ile Lys Glu His Leu His Ile Val Lys Arg
435 440 445

Asp Ile Asp Asn Leu Val Gln Arg Asn Met Pro Ser Asn Glu Lys Pro
450 455 460

Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser Cys Leu Ser Thr Val His
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ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc ccc act aca cct	96
Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro	
20 25 30	
ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg gat ata act gac	144
Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp	
35 40 45	
ggc aac agt gaa cat ctc aag cgg gag cat tcg ctc att aag ccc tac	192
Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr	
50 55 60	
caa ggg gtc ggt tcc agc tct atg ccc ctc tgg gac ttc cag ggc agc	240
Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser	
65 70 75 80	
act atg ctc acg agc cag tac gta cgt ctg acc cct gac gag cgc agc	288
Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser	
85 90 95	
aaa gag ggc tct atc tgg aac cac cag cgg tgc ttc ctc aaa gac tgg	336
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp	
100 105 110	
gaa atg cac gtc cac ttc aaa gtc cac ggc aca ggg aag aag aac ctc	384
Glu Met His Val His Phe Lys Val His Gly Thr Gly Lys Lys Asn Leu	
115 120 125	
cat gga gac ggc atc gcc ttg tgg tac acc cgg gac cgc ctc gtg cca	432
His Gly Asp Gly Ile Ala Leu Trp Tyr Thr Arg Asp Arg Leu Val Pro	
130 135 140	
ggg cct gtg ttt gga agc aaa gat aac ttc cac ggc tta gcc atc ttc	480

Gly Pro Val Phe Gly Ser Lys Asp Asn Phe His Gly Leu Ala Ile Phe
 145 150 155 160

ctg gac acc tac ccc aat gat gag acc act gag cgc gtg ttc ccg tac 528
 Leu Asp Thr Tyr Pro Asn Asp Glu Thr Thr Glu Arg Val Phe Pro Tyr
 165 170 175

atc tcg gtg atg gtg aac aat ggc tcc ctg tcc tac gac cac agc aag 576
 Ile Ser Val Met Val Asn Asn Gly Ser Leu Ser Tyr Asp His Ser Lys
 180 185 190

gat ggg cgc tgg acc gag ctg gcg ggc tgc acg gct gac ttc cgc aac 624
 Asp Gly Arg Trp Thr Glu Leu Ala Gly Cys Thr Ala Asp Phe Arg Asn
 195 200 205

cgc gat cac gac acc ttc ctg gct gtg cgc tac tcc cgg ggc cgt ctg 672
 Arg Asp His Asp Thr Phe Leu Ala Val Arg Tyr Ser Arg Gly Arg Leu
 210 215 220

acg gtg atg acc gac ctg gag gac aag aac gag tgg aag aac tgc att 720
 Thr Val Met Thr Asp Leu Glu Asp Lys Asn Glu Trp Lys Asn Cys Ile
 225 230 235 240

gac atc acg gga gtg cgc ctg ccc acc ggc tac tac ttc ggg gcc tcc 768
 Asp Ile Thr Gly Val Arg Leu Pro Thr Gly Tyr Tyr Phe Gly Ala Ser
 245 250 255

gcc ggc acc ggc gac ctg tct gac aat cat gac atc atc tcc atg aag 816
 Ala Gly Thr Gly Asp Leu Ser Asp Asn His Asp Ile Ile Ser Met Lys
 260 265 270

ctg ttc cag ctg atg gtg gag cac acg ccc gac gag gag agc atc gac 864
 Leu Phe Gln Leu Met Val Glu His Thr Pro Asp Glu Glu Ser Ile Asp
 275 280 285

tgg acc aag atc gag ccc agc gtc aac ttc ctc aag tcg ccc aaa gac 912
 Trp Thr Lys Ile Glu Pro Ser Val Asn Phe Leu Lys Ser Pro Lys Asp
 290 295 300

aac gtg gac gac ccc acg ggg aac ttc cgc agc ggg ccc ctg acg ggg 960
 Asn Val Asp Asp Pro Thr Gly Asn Phe Arg Ser Gly Pro Leu Thr Gly
 305 310 315 320

tgg cgg gtg ttc ctg ctg ctg ctg tgc gct ctc ctg ggc atc gtt gtc 1008
 Trp Arg Val Phe Leu Leu Leu Leu Cys Ala Leu Leu Gly Ile Val Val

325	330	335	
tgc gcc gtg gtg ggg gcc gtg gtg ttc cag aag cgg cag gag cgg aac			1056
Cys Ala Val Val Gly Ala Val Val Phe Gln Lys Arg Gln Glu Arg Asn			
340	345	350	
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Lys Arg Phe Tyr			
355			
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actgtttcaa ataaatgatt aaagtatatt catacatttt gcttcttgcc cagcagggac 1231			
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Leu Phe Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp			
35	40	45	
Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr			
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Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser			
65	70	75	80
Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser			
85	90	95	
Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp			

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Glu	Met	His	Val	His	Phe	Lys	Val	His	Gly	Thr	Gly	Lys	Lys	Asn	Leu	
115					120					125						
His	Gly	Asp	Gly	Ile	Ala	Leu	Trp	Tyr	Thr	Arg	Asp	Arg	Leu	Val	Pro	
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Leu	Asp	Thr	Tyr	Pro	Asn	Asp	Glu	Thr	Thr	Glu	Arg	Val	Phe	Pro	Tyr	
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Ile	Ser	Val	Met	Val	Asn	Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Ser	Lys	
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Arg	Asp	His	Asp	Thr	Phe	Leu	Ala	Val	Arg	Tyr	Ser	Arg	Gly	Arg	Leu	
210					215					220						
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225					230					235					240	
Asp	Ile	Thr	Gly	Val	Arg	Leu	Pro	Thr	Gly	Tyr	Tyr	Phe	Gly	Ala	Ser	
245					250					255						
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Ile	Ile	Ser	Met	Lys	
260					265					270						
Leu	Phe	Gln	Leu	Met	Val	Glu	His	Thr	Pro	Asp	Glu	Glu	Ser	Ile	Asp	
275					280					285						
Trp	Thr	Lys	Ile	Glu	Pro	Ser	Val	Asn	Phe	Leu	Lys	Ser	Pro	Lys	Asp	
290					295					300						
Asn	Val	Asp	Asp	Pro	Thr	Gly	Asn	Phe	Arg	Ser	Gly	Pro	Leu	Thr	Gly	
305					310					315					320	
Trp	Arg	Val	Phe	Leu	Leu	Leu	Leu	Cys	Ala	Leu	Leu	Gly	Ile	Val	Val	
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340

345

350

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<213> Artificial Sequence

<220>
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oligonucleotide

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<210> 6
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<212> DNA
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<210> 13

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32

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oligonucleotide

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<212> PRT

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